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African Rices Genome Projects : GLASS and Irigin

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The GLASS project (GLAberrima ASSembly), jointly between IRD and AfricaRice, aims to sequence de novo the two African NERICA parents, CG14 and TOG5681, representing the two opposite of the glaberrima variability. For that purpose we choose an hybrid approach combining the Illumina high-quality short reads and the PacificBioscience Long Reads technology.
Tests were performed using Illumina data on TOG 5307 and TOG5681, using AbySS short-reads assembler, with 19x and 25x total data respectively. For TOG5307, we obtained 153'774 contigs (minimum size of 200b), mean size of 1.5 kb (N50 = 2.4kb, N90 = 637b). On TOG5681, we obtained 97'196 contigs (minimum size 200b), with a mean size of 2.8kb (N50 = 5kb, N90 = 1.3 kb). The overall assembly for each genome is of 0.56x for TOG5307 and of 0.69x for TOG5681. Just adding +6x of Illumina data almost doubled the assembly efficiency. PacBio data test on C2 and XL kits were also perfomed for CG14 data, providing respectively 143'456 and 99'488 contigs (mean size of 3140b and 3184b), with a 1.12x and 0.79x coverage. The C2 10x sequencing in PacBio for CG14 and TOG5681, and the 60x sequencing in Illumina for each is on the way.
The annotation will be transfered from the Nipponbare MSU7.0 reference genome using tools such as QOD (Mancheron et al, 2010) and BLAST/BLAT based scripts. These sequences will be immediatly available for the whole community without restriction.
The IRIGIN project from France Genomique (International RIce Genomic INitiative, http://irigin.org) is headed by IRD and CIRAD, and aimed to provide valuable genetic stocks genomic data in the frame of GriSP. African rice (300 O. glaberrima and 100 O. barthii) will be deeply resequenced (25x) and aligned on their reference (from the GLASS project). In the same time , NAMs population (indica x tropical japonica) from AfricaRice and CIAT will be genotyped (using low-coverage sequencing), to provide to the rice community the best genetic map ever created in plants, with the highest level of coverage ever seen. Thousand of terabytes of raw data and billions of polymorphic data will be gathered within this project, and will be distributed to the whole rice community as soon as possible.

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Meeting Information

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